



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/663,158

DATE: 08/04/2004

TIME: 08:22:56

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\08042004\J663158.raw

3 <110> APPLICANT: Desauvage, Frederic  
 4 Grewal, Iqbal  
 5 Gurney, Austin L.  
 7 <120> TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCCR  
 9 <130> FILE REFERENCE: 11669.123USC1  
 11 <140> CURRENT APPLICATION NUMBER: US 10/663,158  
 12 <141> CURRENT FILING DATE: 2003-09-15  
 14 <150> PRIOR APPLICATION NUMBER: US 09/692,504  
 15 <151> PRIOR FILING DATE: 2000-10-18  
 17 <150> PRIOR APPLICATION NUMBER: US 60/160,542  
 18 <151> PRIOR FILING DATE: 1999-10-20  
 20 <160> NUMBER OF SEQ ID NOS: 16  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 636  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Homo sapiens  
 29 <400> SEQUENCE: 1  
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 32 1 5 10 15  
 35 Leu Ala Leu Leu Pro Leu Leu Trp Val Leu Phe Gln Arg Thr Arg Pro  
 36 20 25 30  
 39 Gln Gly Ser Ala Gly Pro Leu Gln Cys Tyr Gly Val Gly Pro Leu Gly  
 40 35 40 45  
 43 Asp Leu Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu Gly Ala Pro Ser  
 44 50 55 60  
 47 Glu Leu His Leu Gln Ser Gln Lys Tyr Arg Ser Asn Lys Thr Gln Thr  
 48 65 70 75 80  
 51 Val Ala Val Ala Ala Gly Arg Ser Trp Val Ala Ile Pro Arg Glu Gln  
 52 85 90 95  
 55 Leu Thr Met Ser Asp Lys Leu Leu Val Trp Gly Thr Lys Ala Gly Gln  
 56 100 105 110  
 59 Pro Leu Trp Pro Pro Val Phe Val Asn Leu Glu Thr Gln Met Lys Pro  
 60 115 120 125  
 63 Asn Ala Pro Arg Leu Gly Pro Asp Val Asp Phe Ser Glu Asp Asp Pro  
 64 130 135 140  
 67 Leu Glu Ala Thr Val His Trp Ala Pro Pro Thr Trp Pro Ser His Lys  
 68 145 150 155 160  
 71 Val Leu Ile Cys Gln Phe His Tyr Arg Arg Cys Gln Glu Ala Ala Trp  
 72 165 170 175  
 75 Thr Leu Leu Glu Pro Glu Leu Lys Thr Ile Pro Leu Thr Pro Val Glu  
 76 180 185 190  
 79 Ile Gln Asp Leu Glu Leu Ala Thr Gly Tyr Lys Val Tyr Gly Arg Cys



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80	195	200	205
83	Arg Met Glu Lys Glu Glu Asp Leu Trp Gly Glu Trp Ser Pro Ile Leu		
84	210	215	220
87	Ser Phe Gln Thr Pro Pro Ser Ala Pro Lys Asp Val Trp Val Ser Gly		
88	225	230	235 240
91	Asn Leu Cys Gly Thr Pro Gly Gly Glu Glu Pro Leu Leu Leu Trp Lys		
92	245	250	255
95	Ala Pro Gly Pro Cys Val Gln Val Ser Tyr Lys Val Trp Phe Trp Val		
96	260	265	270
99	Gly Gly Arg Glu Leu Ser Pro Glu Gly Ile Thr Cys Cys Cys Ser Leu		
100	275	280	285
103	Ile Pro Ser Gly Ala Glu Trp Ala Arg Val Ser Ala Val Asn Ala Thr		
104	290	295	300
107	Ser Trp Glu Pro Leu Thr Asn Leu Ser Leu Val Cys Leu Asp Ser Ala		
108	305	310	315 320
111	Ser Ala Pro Arg Ser Val Ala Val Ser Ser Ile Ala Gly Ser Thr Glu		
112	325	330	335
115	Leu Leu Val Thr Trp Gln Pro Gly Pro Gly Glu Pro Leu Glu His Val		
116	340	345	350
119	Val Asp Trp Ala Arg Asp Gly Asp Pro Leu Glu Lys Leu Asn Trp Val		
120	355	360	365
123	Arg Leu Pro Pro Gly Asn Leu Ser Ala Leu Leu Pro Gly Asn Phe Thr		
124	370	375	380
127	Val Gly Val Pro Tyr Arg Ile Thr Val Thr Ala Val Ser Ala Ser Gly		
128	385	390	395 400
131	Leu Ala Ser Ala Ser Ser Val Trp Gly Phe Arg Glu Glu Leu Ala Pro		
132	405	410	415
135	Leu Val Gly Pro Thr Leu Trp Arg Leu Gln Asp Ala Pro Pro Gly Thr		
136	420	425	430
139	Pro Ala Ile Ala Trp Gly Glu Val Pro Arg His Gln Leu Arg Gly His		
140	435	440	445
143	Leu Thr His Tyr Thr Leu Cys Ala Gln Ser Gly Thr Ser Pro Ser Val		
144	450	455	460
147	Cys Met Asn Val Ser Gly Asn Thr Gln Ser Val Thr Leu Pro Asp Leu		
148	465	470	475 480
151	Pro Trp Gly Pro Cys Glu Leu Trp Val Thr Ala Ser Thr Ile Ala Gly		
152	485	490	495
155	Gln Gly Pro Pro Gly Pro Ile Leu Arg Leu His Leu Pro Asp Asn Thr		
156	500	505	510
159	Leu Arg Trp Lys Val Leu Pro Gly Ile Leu Phe Leu Trp Gly Leu Phe		
160	515	520	525
163	Leu Leu Gly Cys Gly Leu Ser Leu Ala Thr Ser Gly Arg Cys Tyr His		
164	530	535	540
167	Leu Arg His Lys Val Leu Pro Arg Trp Val Trp Glu Lys Val Pro Asp		
168	545	550	555 560
171	Pro Ala Asn Ser Ser Ser Gly Gln Pro His Met Glu Gln Val Pro Glu		
172	565	570	575
175	Ala Gln Pro Leu Gly Asp Leu Pro Ile Leu Glu Val Glu Glu Met Glu		
176	580	585	590

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179 Pro Pro Pro Val Met Glu Ser Ser Gln Pro Ala Gln Ala Thr Ala Pro
180      595      600      605
183 Leu Asp Ser Gly Tyr Glu Lys His Phe Leu Pro Thr Pro Glu Glu Leu
184      610      615      620
187 Gly Leu Leu Gly Pro Pro Arg Pro Gln Val Leu Ala
188 625      630      635
191 <210> SEQ ID NO: 2
192 <211> LENGTH: 623
193 <212> TYPE: PRT
194 <213> ORGANISM: Mus musculus
196 <400> SEQUENCE: 2
198 Met Asn Arg Leu Arg Val Ala Arg Leu Thr Pro Leu Glu Leu Leu Leu
199 1      5      10      15
202 Ser Leu Met Ser Leu Leu Leu Gly Thr Arg Pro His Gly Ser Pro Gly
203      20      25      30
206 Pro Leu Gln Cys Tyr Ser Val Gly Pro Leu Gly Ile Leu Asn Cys Ser
207      35      40      45
210 Trp Glu Pro Leu Gly Asp Leu Glu Thr Pro Pro Val Leu Tyr His Gln
211      50      55      60
214 Ser Gln Lys Tyr His Pro Asn Arg Val Trp Glu Val Lys Val Pro Ser
215 65      70      75      80
218 Lys Gln Ser Trp Val Thr Ile Pro Arg Glu Gln Phe Thr Met Ala Asp
219      85      90      95
222 Lys Leu Leu Ile Trp Gly Thr Gln Lys Gly Arg Pro Leu Trp Ser Ser
223      100     105     110
226 Val Ser Val Asn Leu Glu Thr Gln Met Lys Pro Asp Thr Pro Gln Ile
227      115     120     125
230 Phe Ser Gln Val Asp Ile Ser Glu Glu Ala Thr Leu Glu Ala Thr Val
231      130     135     140
234 Gln Trp Ala Pro Pro Val Trp Pro Pro Gln Lys Ala Leu Thr Cys Gln
235 145     150     155     160
238 Phe Arg Tyr Lys Glu Cys Gln Ala Glu Ala Trp Thr Arg Leu Glu Pro
239      165     170     175
242 Gln Leu Lys Thr Asp Gly Leu Thr Pro Val Glu Met Gln Asn Leu Glu
243      180     185     190
246 Pro Gly Thr Cys Tyr Gln Val Ser Gly Arg Cys Gln Val Glu Asn Gly
247      195     200     205
250 Tyr Pro Trp Gly Glu Trp Ser Ser Pro Leu Ser Phe Gln Thr Pro Phe
251      210     215     220
254 Leu Asp Pro Glu Asp Val Trp Val Ser Gly Thr Val Cys Glu Thr Ser
255 225     230     235     240
258 Gly Lys Arg Ala Ala Leu Leu Val Trp Lys Asp Pro Arg Pro Cys Val
259      245     250     255
262 Gln Val Thr Tyr Thr Val Trp Phe Gly Ala Gly Asp Ile Thr Thr Thr
263      260     265     270
266 Gln Glu Glu Val Pro Cys Cys Lys Ser Pro Val Pro Ala Trp Met Glu
267      275     280     285
270 Trp Ala Val Val Ser Pro Gly Asn Ser Thr Ser Trp Val Pro Pro Thr
271      290     295     300

```

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```

274 Asn Leu Ser Leu Val Cys Leu Ala Pro Glu Ser Ala Pro Cys Asp Val
275 305                      310                      315                      320
278 Gly Val Ser Ser Ala Asp Gly Ser Pro Gly Ile Lys Val Thr Trp Lys
279                      325                      330                      335
282 Gln Gly Thr Arg Lys Pro Leu Glu Tyr Val Val Asp Trp Ala Gln Asp
283                      340                      345                      350
286 Gly Asp Ser Leu Asp Lys Leu Asn Trp Thr Arg Leu Pro Pro Gly Asn
287                      355                      360                      365
290 Leu Ser Thr Leu Leu Pro Gly Glu Phe Lys Gly Gly Val Pro Tyr Arg
291                      370                      375                      380
294 Ile Thr Val Thr Ala Val Tyr Ser Gly Gly Leu Ala Ala Ala Pro Ser
295 385                      390                      395                      400
298 Val Trp Gly Phe Arg Glu Glu Leu Val Pro Leu Ala Gly Pro Ala Val
299                      405                      410                      415
302 Trp Arg Leu Pro Asp Asp Pro Pro Gly Thr Pro Val Val Ala Trp Gly
303                      420                      425                      430
306 Glu Val Pro Arg His Gln Leu Arg Gly Gln Ala Thr His Tyr Thr Phe
307                      435                      440                      445
310 Cys Ile Gln Ser Arg Gly Leu Ser Thr Val Cys Arg Asn Val Ser Ser
311                      450                      455                      460
314 Gln Thr Gln Thr Ala Thr Leu Pro Asn Leu His Ser Gly Ser Phe Lys
315 465                      470                      475                      480
318 Leu Trp Val Thr Val Ser Thr Val Ala Gly Gln Gly Pro Pro Gly Pro
319                      485                      490                      495
322 Asp Leu Ser Leu His Leu Pro Asp Asn Arg Ile Arg Trp Lys Ala Leu
323                      500                      505                      510
326 Pro Trp Phe Leu Ser Leu Trp Gly Leu Leu Leu Met Gly Cys Gly Leu
327                      515                      520                      525
330 Ser Leu Ala Ser Thr Arg Cys Leu Gln Ala Arg Cys Leu His Trp Arg
331                      530                      535                      540
334 His Lys Leu Leu Pro Gln Trp Ile Trp Glu Arg Val Pro Asp Pro Ala
335 545                      550                      555                      560
338 Asn Ser Asn Ser Gly Gln Pro Tyr Ile Lys Glu Val Ser Leu Pro Gln
339                      565                      570                      575
342 Pro Pro Lys Asp Gly Pro Ile Leu Glu Val Glu Glu Val Glu Leu Gln
343                      580                      585                      590
346 Pro Val Val Glu Ser Pro Lys Ala Ser Ala Pro Ile Tyr Ser Gly Tyr
347                      595                      600                      605
350 Glu Lys His Phe Leu Pro Thr Pro Glu Glu Leu Gly Leu Leu Val
351                      610                      615                      620
354 <210> SEQ ID NO: 3
355 <211> LENGTH: 2646
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
359 <220> FEATURE:
360 <221> NAME/KEY: misc_feature
361 <222> LOCATION: (2433)..(2433)
362 <223> OTHER INFORMATION: n is a, c, t, or g
365 <400> SEQUENCE: 3

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DATE: 08/04/2004

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TIME: 08:22:56

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\08042004\J663158.raw

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366 gtgggttcgg cttcccgttg cgcctcgggg gctgtaccca gagctcgaag aggagcagcg      60
368 cggcccgcac ccggcaaggc tgggccggac tcggggctcc cgagggacgc catgcgggga      120
370 ggcaggggcg cccctttctg gctgtggccg ctgcccgaagc tggcgtgct gcctctgttg      180
372 tgggtgcttt tccagcggac gcgtccccag ggcagcgccg ggccactgca gtgctacgga      240
374 gttggaccct tgggcgactt gaactgctcg tgggagcctc ttggggacct gggagcccc      300
376 tccgagttac acctccagag ccaaaagtac cgttccaaca aaaccagac tgtggcagtg      360
378 gcagccggac ggagctgggt ggccattcct cgggaacagc tcaccatgtc tgacaaactc      420
380 cttgtctggg gactaaggc aggccagcct ctctggcccc ccgtcttcgt gaacctagaa      480
382 acccaaatga agccaaacgc cccccggctg ggccctgacg tggacttttc cgaggatgac      540
384 cccctggagg ccactgtcca ttgggccccca cctacatggc catctcataa agttctgatc      600
386 tgccagttcc actaccgaag atgtcaggag gcggcctgga ccctgctgga accggagctg      660
388 aagaccatac ccctgacccc tgttgagatc caagatttgg agctagccac tggctacaaa      720
390 gtgtatggcc gctgccggat ggagaaagaa gaggatttgt ggggagagtg gagccccatt      780
392 ttgtccttcc agacaccgcc ttctgctcca aaagatgtgt gggatcagg gaacctctgt      840
394 gggacgcctg gaggagagga acctttgctt ctatggaagg cccaggggcc ctgtgtgcag      900
396 gtgagctaca aagtctggtt ctgggttggg ggtcgtgagc tgagtccaga aggaattacc      960
398 tgctgctgct ccctaattcc cagtggggcg gagtgggcca ggggtgtccg tgtcaacgcc     1020
400 acaagctggg agcctctcac caacctctct ttggtctgct tggattcagc ctctgcccc     1080
402 cgtagcgtgg cagtcagcag catcgtggg agcacggagc tactggtgac ctggcaaccg     1140
404 gggcctgggg aaccactgga gcatgtagtg gactgggctc gagatgggga cccctggag     1200
406 aaactcaact gggtcgggct tccccctggg aacctcagtg ctctgttacc agggaatttc     1260
408 actgtcgggg tcccctatcg aatcactgtg accgcagctc ctgcttcagg cttggcctct     1320
410 gcatcctccg tctggggggt cagggaggaa ttagcaccce tagtggggcc aacgctttgg     1380
412 cgactccaag atgcccctcc agggaccccc gccatagcgt ggggagaggt cccaaggcac     1440
414 cagcttcgag gccacctcac ccactacacc ttgtgtgcac agagtggaac cagcccctcc     1500
416 gtctgcatga atgtgagtgg caacacacag agtgtcacc tgctgacct tccttggggg     1560
418 ccctgtgagc tgtgggtgac agcatctacc atcgtggac agggccctcc tggteccatc     1620
420 ctccggcttc atctaccaga taacaccttg aggtggaaag ttctgccggg catcctattc     1680
422 ttgtgggggt tgttcctggt ggggtgtggc ctgagcctgg ccacctctgg aaggtgctac     1740
424 cacctaaggc acaaagtgtt gcccgcgtgg gtctgggaga aagtctctga tcctgccaac     1800
426 agcagttcag gccagcccca catggagcaa gtacctgagg ccagccctt tggggacttg     1860
428 cccatcctgg aagtggagga gatggagccc ccgcccgtta tggagtctc ccagcccgcc     1920
430 cagggcaccg ccccgcttga ctctgggtat gagaagcact tcctgccac acctgaggag     1980
432 ctgggccttc tggggccccc caggccacag gttctggcct gaaccacacg tctggctggg     2040
434 ggctgccagc caggctagag ggatgctcat gcaggttgca cccagtcct ggattagccc     2100
436 tcttgatgga tgaagacact gaggactcag agaggctgag tacttacct gaggacacc     2160
438 agccaggcag agctgggatt gaaggacccc tatagagaag ggcttggccc ccatggggaa     2220
440 gacacggatg gaaggtggag caaaggaaaa tacatgaaat tgagagtggc agctgcctgc     2280
442 caaaatctgt tccgctgtaa cagaactgaa tttggacccc agcacagtgg ctcacgcctg     2340
444 taatcccagc actttggcag gccaaagggtg aaggatcact tagagctagg agtttgagac     2400
W--> 446 cagcctgggc aatatagcaa gaccctcac tanaaaaata aaacatcaaa aacaaaaaca     2460
448 attagctggg catgatggca cacacctgta gtccgagcca cttgggaggc tgaggtggga     2520
450 ggatcggttg agcccaggag ttccaagctg caggacctc tgattgcacc actgcactcc     2580
452 aggtgggta acagaatgag accttatctc aaaaataaac aaactaataa aaaaaaaaaa     2640
454 aaaaaa
457 <210> SEQ ID NO: 4
458 <211> LENGTH: 2005
459 <212> TYPE: DNA
460 <213> ORGANISM: Mus musculus

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/663,158

DATE: 08/04/2004  
TIME: 08:22:57

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF4\08042004\J663158.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2433

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/663,158

DATE: 08/04/2004

TIME: 08:22:57

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\08042004\J663158.raw

L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2400